



Review on biology and epidemiology of maize lethal necrosis disease

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Abstract

Maize (*Zea mays L.*) is one of the most important and staple food and source of income and livelihood in Sub-Saharan Africa. However, its productivity remains low as compared to the mean yields in the developed world. These may due to several limiting factors among these, pests and diseases may have great role. Maize lethal necrosis disease (MLND) is one of the most destructive diseases with higher yield losses and the occurrence of disease has been reported in various parts of the world. The disease is mainly caused by co-infection between Maize Dwarf Mosaic Virus (MCMV) and Sugarcane Chlorotic Mosaic Virus (SCMV). Proper identification of the causative agent causing the suspected disease is the major aim of controlling diseases. Even though symptomatology is one key of disease identification, as a result of different circumstances like varying in genotype, time of infection, environmental conditions and the potential for multiple infections, visual observation judgments should be assured through serological assays. The aim of this review article was to provide an overview on the current knowledge on MLND causative agents, genetic architecture and mechanisms by which synergism occur.

Keywords: DNA, RNA, Occurrence, Particles, Symptomology, Synergistic.

1. Introduction

Maize (*Zea mays L.*) is a major staple food and source of income and livelihood for the majority of smallholder farming communities in sub-Saharan Africa (Sharma and Misra, 2011). However, maize productivity in Africa remains relatively low compared to average yields in Asia and the developed world (Chauvin *et al.*, 2012; Macauley and Ramadjita, 2015). These may due to drought, low soil fertility, pests and diseases. Among diseases, MLND is the most destructive disease with higher yield losses (Xie *et al.*, 2016; Yang *et al.*, 2017).

The disease was first identified in Kenya in 2012 (Wangai *et al.*, 2012) and subsequently in Rwanda (Adams *et al.*, 2014), the Democratic Republic of Congo (Lukanda *et al.*, 2014), and in the border districts of Uganda. In July 2014, the disease was detected from maize plants exhibiting severe yellowing and chlorotic mottle symptoms in Ethiopia (Mahuku *et al.*, 2015a), signifying the presence of MLND disease in the country. The outbreak and rapid spread of MLND disease in East Africa has emerged as a big challenge to maize production and has significantly affected the productivity of the crop in the region. The disease can cause significant yield reduction, and loss of grain quality and food supplies. In highly affected regions, yield losses of 90-100% may occur (Adams *et al.*, 2014).

Occurrence of MLND has been reported in various parts of the world and is caused by synergistic interactions between Maize Chlorotic Mottle Virus (MCMV) (family Tombusviridae, genus Machlomovirus) and any of Sugarcane Chlorotic Mosaic Virus (SCMV), Maize Dwarf Mosaic Virus (MDMV) (family Potyviridae, genus Potyvirus) or Wheat Streak Mosaic Virus (WSMV) (family Potyviridae, genus Tritimovirus) (Xie *et al.*, 2016; Wang *et al.*, 2017). In Africa, the disease is mainly caused by co-infection by MCMV and SCMV (Adams *et al.*, 2014). Both MCMV and SCMV synergistically interact with one another such that the two comfortably survive in the infected maize plant (Xie *et al.*, 2016). Any of the two viruses can infect the maize plant before the other or both can infect the plant at the same time (Gowda *et al.*, 2015; Xie *et al.*, 2016). In Ethiopia, both MCMV and SCMV were found to cause MLND symptoms in 2014 either alone or in mixed infections (Mahuku *et al.*, 2015a).

Plants affected by MLND shows symptoms like stunting, necrosis, mottling, streak and mosaic pattern, elongated yellow streaks parallel to leaf veins, streaks may coalesce to create chlorotic mottling. Chlorotic mottling may be followed by leaf necrosis which may lead to “dead heart” symptom and plant death (Wangai et al., 2012), premature aging of the plants, failure to tassel and sterility in male plants, malformed or no ears (Godon et al., 1984), failure of cobs to put on grains and rotting of cobs. Even though symptomatology is one key of disease identification, as a result of different circumstances like varying in genotype, time of infection, environmental conditions and the potential for multiple infections, visual observation judgments should be assured through serological assays such as enzyme-linked immunosorbent assay (ELISA) and/or molecular tests such as reverse-transcription polymerase chain reaction (RT-PCR) (Mahuku et al., 2015a; Mengistu, 2016). This review was undertaken to elucidate the current knowledge on MLND causative viruses, genetic architecture and mechanisms by which synergism occurs. The information gathered may be useful for developing strategies towards improvement of maize for resistance to MLND and appropriate management practices in maize production areas of the world.

2. Biology of MLND of viruses

2.1 Infectious cycle of MLND viruses

The replication processes of viruses determine their life cycle inside the host. MLND viruses are single stranded-positive RNA (ss RNA (+)) and they function both as genome and messenger RNA (mRNA). Unlike DNA viruses, where their reproduction processes begin inside the host nucleus, multiplication processes of the MLND viruses occur in the cytoplasm of the host cells (Mbega *et al.*, 2016). The viruses have the ability to use the metabolic machinery of the host cell to produce their own genetic materials that they can use for multiplication and translation processes necessary for their survival as indicated. Viral particle enters host cell through wounds made mechanically or by vectors on the cell wall or by deposition into an ovule by an infected pollen grain (Xie *et al.*, 2016).

2.2 Interactions between MLND viruses and vectors

Majority of plant viruses depend on their vectors for plant-plant movement, presumably, due to lack of cellular receptors and inability to break the cell wall (Cann, 2005). MLND viruses are transmitted by phloem-feeding vectors (Sharma and Misra, 2011). The interactions between SCMV and MCMV and their vectors depend on non-persistent transmission facilitated by capsid and helper component proteins (Kiruwa *et al.*, 2016; Mbega *et al.*, 2016). The MLND viruses concentrate within the phloem of the infected maize plant for them to be able to move long distances within the plant systems (Mbega *et al.*, 2016).

2.3 Methods of MLND detection

The following methods have been effectively employed to identify and determine the molecular properties of MLND viruses.

2.3.1 Symptomatology

MLND is the phrase used to describe a variety of symptoms in maize due to co-infection of the crop by MCMV and SCMV. Use of symptoms and signs related to MLND infections in the field has been very useful in initiating response towards MLND control. Use of symptoms to tell the presence of MLND is simple because it depends on phenotypic observations in the field. Even though symptomatology is one key of disease identification, as a result of different circumstances like varying in genotype, time of infection, environmental conditions and the potential for multiple infections, visual observation judgments should be assured through serological assays such as ELISA and/or molecular tests such as RT-PCR (Mahuku *et al.*, 2015a; Mengistu, 2016; Wangai *et al.*, 2012).

2.3.2 Serological methods/ELISA

Identification and detection of viruses based on specificity of the antigen–antibody reaction is well documented. ELISA method, introduced by Clark and Adams (1977), is easy to apply and is commonly used for detection of MLND viruses (Mezzalama, 2015). Effective and low-cost ELISA kits including double antibody sandwich ELISA (DAS-ELISA) technique are commercially available for detection of MCMV and SCMV. DAS-ELISA results depend on the chemical reactions between antigens and antibodies. The virus CP contains antigens (antigenic determinants) which react with the antibodies in specific manner. Positive reactions occur when the antigenic determinant (epitope) reacts with the coding region (paratope) of the antibody resulting into yellow coloration (Mezzalama, 2015, Xie *et al.*, 2016).

2.3.3 Molecular methods/RT-PCR

The technique includes dot blot hybridization/slot blot hybridization, polymerase chain reaction (PCR), and nucleic acid hybridization with radiolabeled and non-radio-labelled probes, and DNA/RNA probes (Xie *et al.*, 2016). The screening techniques have been useful for certification of plants free of MLN (Gowda *et al.*, 2015; Xie *et al.*, 2016). The RT-PCR is a sensitive nucleic acid-based technique that increases the small quantity of nucleic acid by amplification. Genomic components of MCMV and SCMV are found in RNA forms which are amplified into complementary DNA (cDNA) using reverse transcriptase. As a result, very small quantities of nucleic acids may be amplified relatively quickly.

2.4 Movement of MLND viruses within the host

Plant viruses have no tool to break host cell wall, therefore, they are introduced into the cytoplasmic cells mechanically by vectors or through wounds, followed by removal of viral coat proteins in the cytoplasm. MLND viruses move from the initial infected cells to the next through PD which is a small opening connecting adjacent cells (Sharma and Misra, 2011). The virus can move as nucleoprotein or as a whole viral particle (virion). Passage of a whole virion across the PD requires enlargement of the PD by formation of tubule along the PD, facilitated by MP and PD receptors called Plasmodesmata Located Proteins (PDL). However, cell-to-cell movement of virus in form of nucleoprotein (mRNA) is non-tubule-guided and the virus genome can easily migrate across the PD supported by MP. The ability of MLND viruses to move from initially infected cells to the next cells results into localized and systemic spread of the viruses within the host system. During long distance movement, MLND viral proteins including MP, CP and VPg interact with the host factors. This allows systemic spread of virus from the infected mesophyll cells to various parts of the plant through the phloem, usually mixed in the solutes. Movement of plant viruses is usually slow due to stiff physiological resistance put by the host systems. It takes about one to few hours for a virus to replicate in one cell before infecting the next cell.

2.5 Signs and recognition of MLND symptoms in the field

Quick and preliminary recognition of presence of vectors and symptoms of MLND disease in the field is to physically observe the common symptoms of the disease. Recognition of MLND in the field is a method based on observation of various symptoms on the maize plant. The method is useful for initiation of studies towards etiology of MLND viruses. As the disease develops, the maize leaves become yellow and dry out from the outside edges towards the midrib and finally, the entire plant dries out and dies (Kiruwa *et al.*, 2016). Dead plants can then be seen scattered across the field among healthy looking plants. Late infection in maize plants lead to non-tasseling and production of poor grain filled cobs (Mahuku *et al.*, 2015a). Availability of thrips and aphids in the fields and alternative hosts (*Paspalum conjugatum*, *Eleusine coracana*, *Sorghum halepense*, etc.) in the surroundings are common signs and indications of potential MLND infections.

3. Epidemiology of MLND Viruses

For an insect-vectored virus disease to emerge in a crop, the virus (es), vectors(s), and a susceptible host must come together in an environment suitable for the disease, with at least one of these factors being new. The causal agents of MLND are MCMV and any of the *Potyvirus*es and *Tritimovirus*. Different isolates of MCMV have been reported, for example, MCMV-P (Peru), MCMV-KS (Kansas) and MCMV-YN (Yunnan), and different unconfirmed strains have been suspected in some parts of Africa including Nigeria, Rwanda, Sao Tome and Principe, Tanzania, Togo, Zambia and Zimbabwe (Sharma and Misra, 2011; Xie *et al.*, 2016).

Virus spread is also enhanced by increase in vector population and favorable weather conditions (Gowda *et al.*, 2015; Yang *et al.*, 2017). Corn thrips (*Frankliniella williamsi*) and aphid (*Rhopalosiphum maidis*) are the common vectors of MLND viruses in Africa and the viruses can survive on different host plants such as cassava, beans, maize, sorghum, onions, rice, peppers (Liu *et al.*, 2017a). Vectors play important roles in the pathogenicity and spread of viruses in plants because they create entry points for the viruses to get into the host cells during feeding.

Additionally, infected soil and seeds have been reported as a reservoir and a means of virus's transmission (Kagoda *et al.*, 2016; Tesfu, 2017). Human activities such as using materials in infected field without closely washing can transmit the disease-causing viruses from infected to uninfected fields. The virus may also be spread through soil and through infected plant debris since the virus can survive in plant residues. Maize production in continuous manner in the same field greatly increases the incidence of the viruses and vectors.

4. Conclusions

Maize lethal necrosis disease (MLND) is a new reported virulent maize disease in Eastern Africa, including Ethiopia. For an insect-vectored virus disease to emerge in a crop, the virus(es), vectors(s), and a susceptible host must come together in an environment suitable for the disease, with at least one of these factors being new. The outbreak and rapid spread of MLND disease has emerged as a big challenge to maize production and has significantly affected the productivity of the crop in the region. It is the result of the co-infection of two or more viruses. An array of diagnostics useful for detection of viruses in the field and the laboratory are available and include the ability to quantify virus titers. Better understanding of the biology and epidemiology of the virus helps us to create the appropriate management practices including host plant resistances. Thus, the gathered information may be useful for developing strategies towards improvement of maize for resistance to MLND and appropriate management practices in maize production areas of the world especially in Eastern African countries since the virus is a new disease.

5. References

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